

1st Round: screening of mutants (full length Ala-scan)

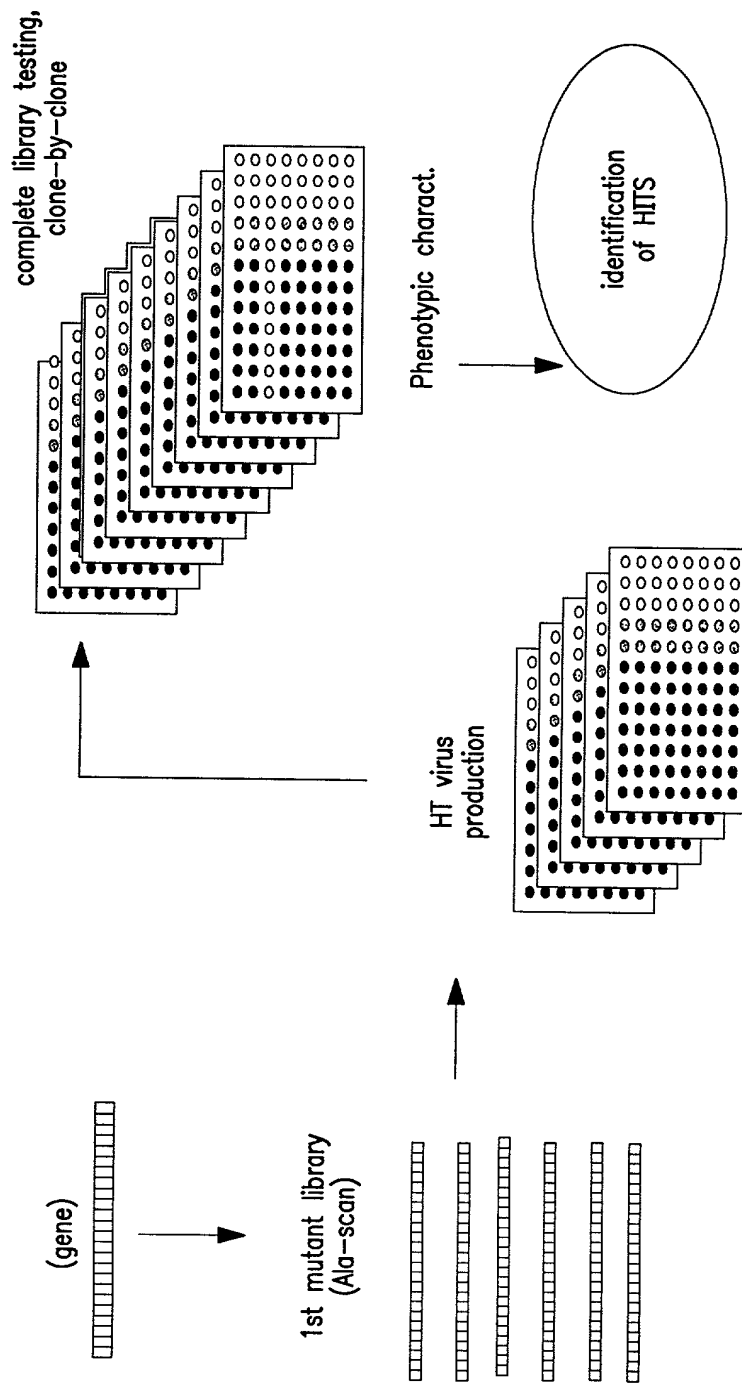


FIG. 1A

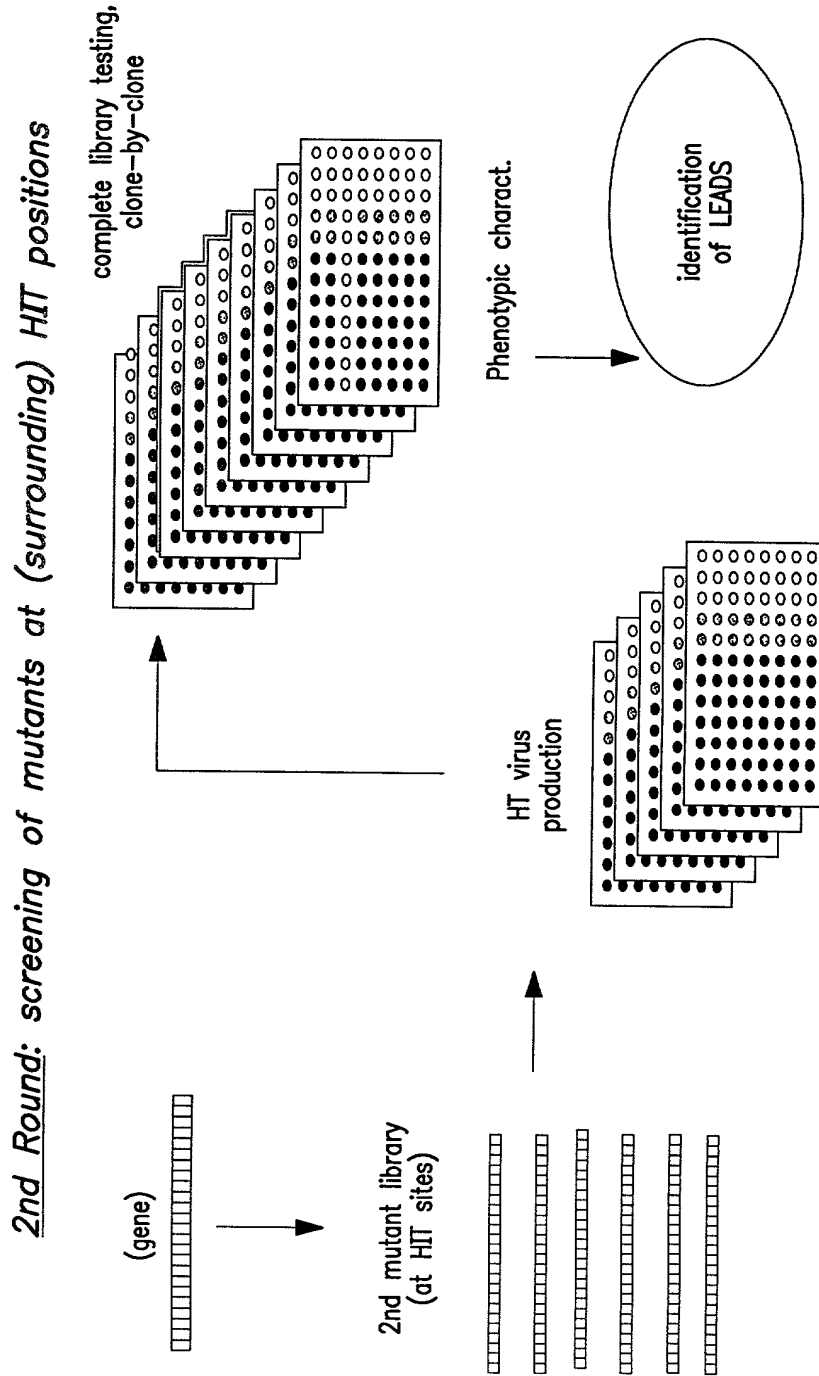


FIG. 1B

3rd Round: screening of recombinants between LEADS

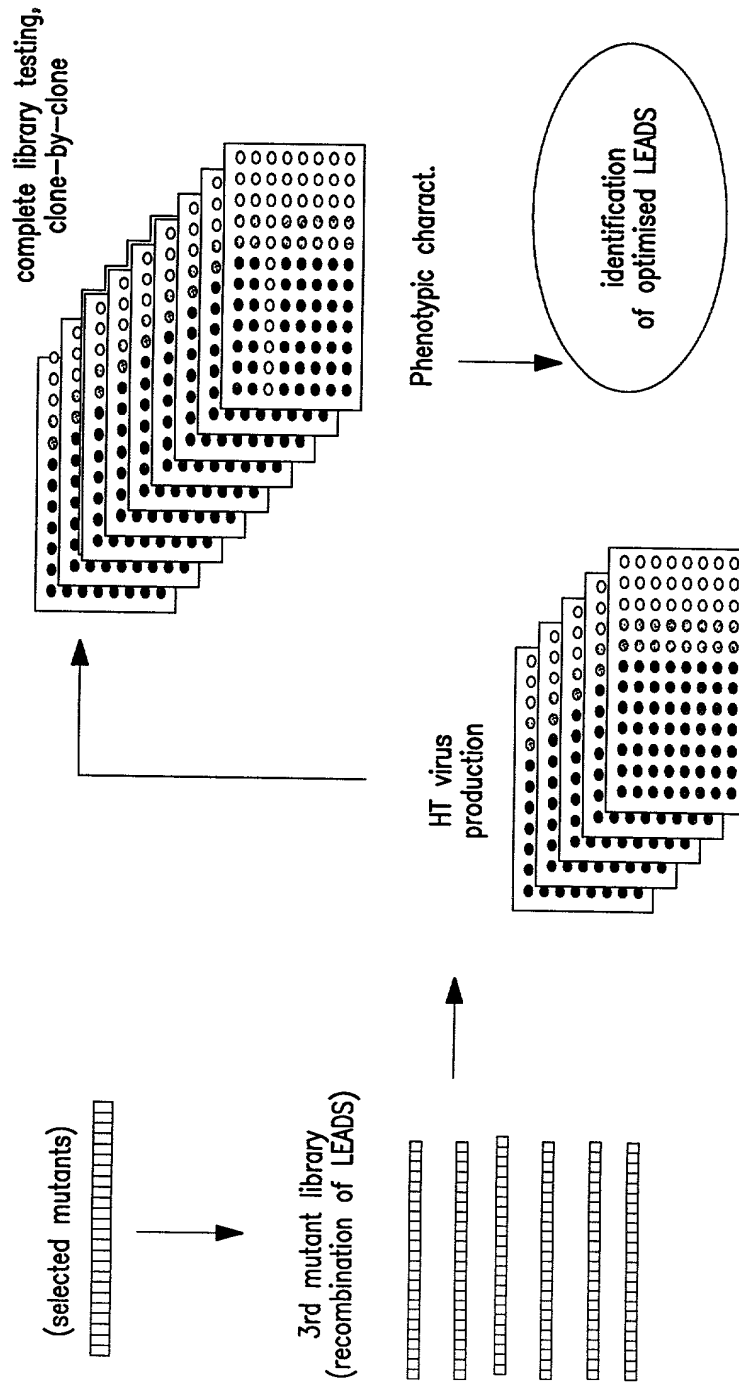


FIG. 1C

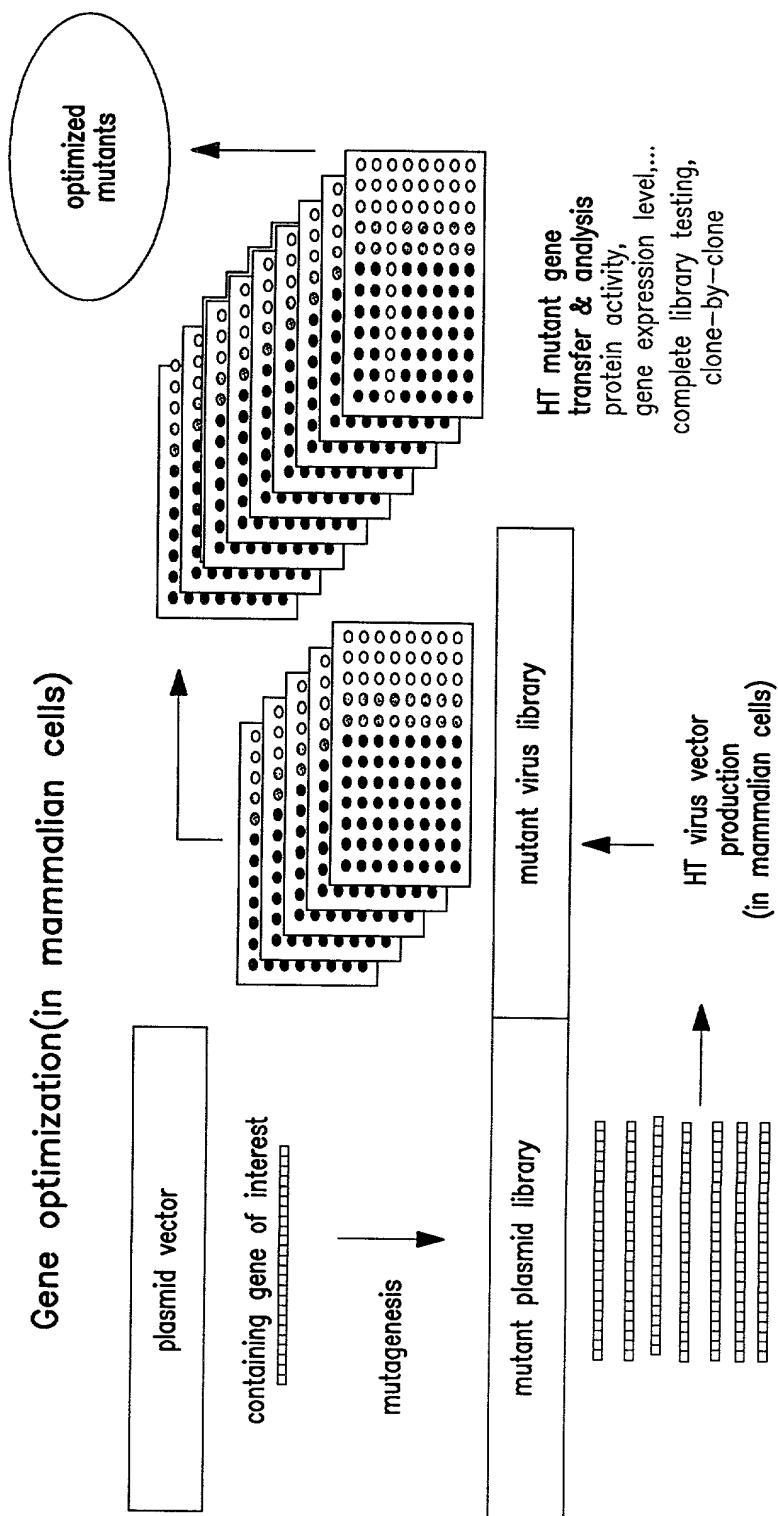


FIG. ID

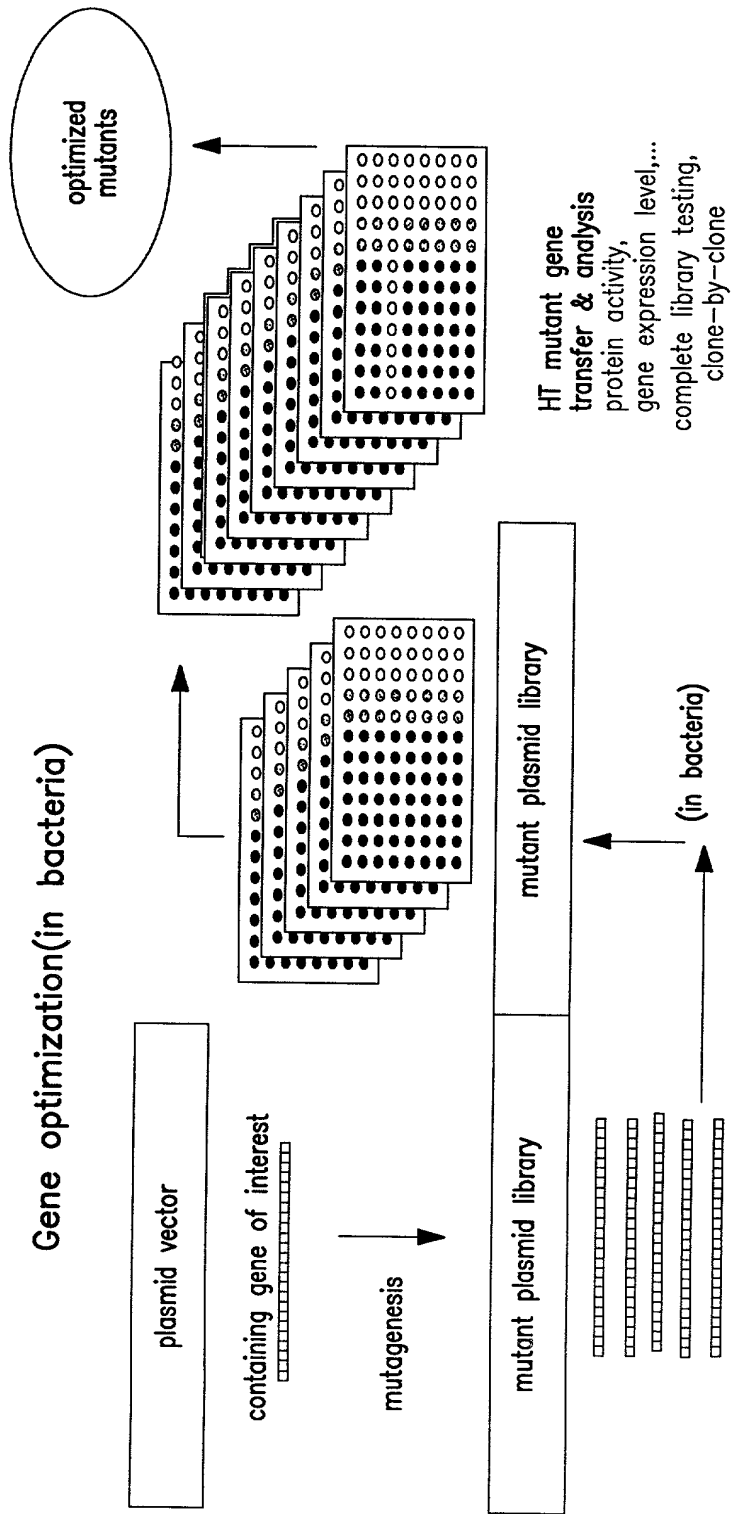


FIG. 1E

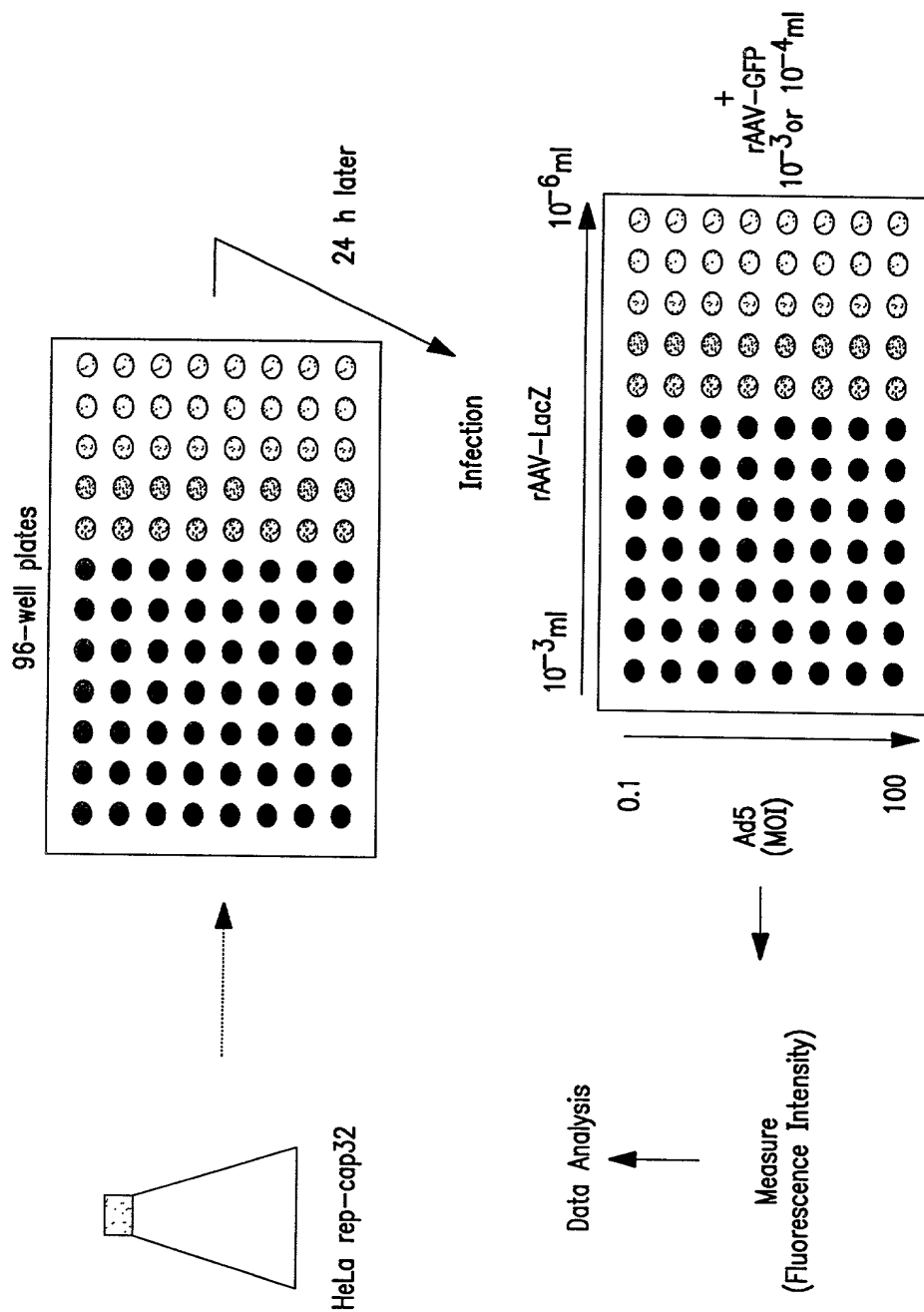


FIG. 2A

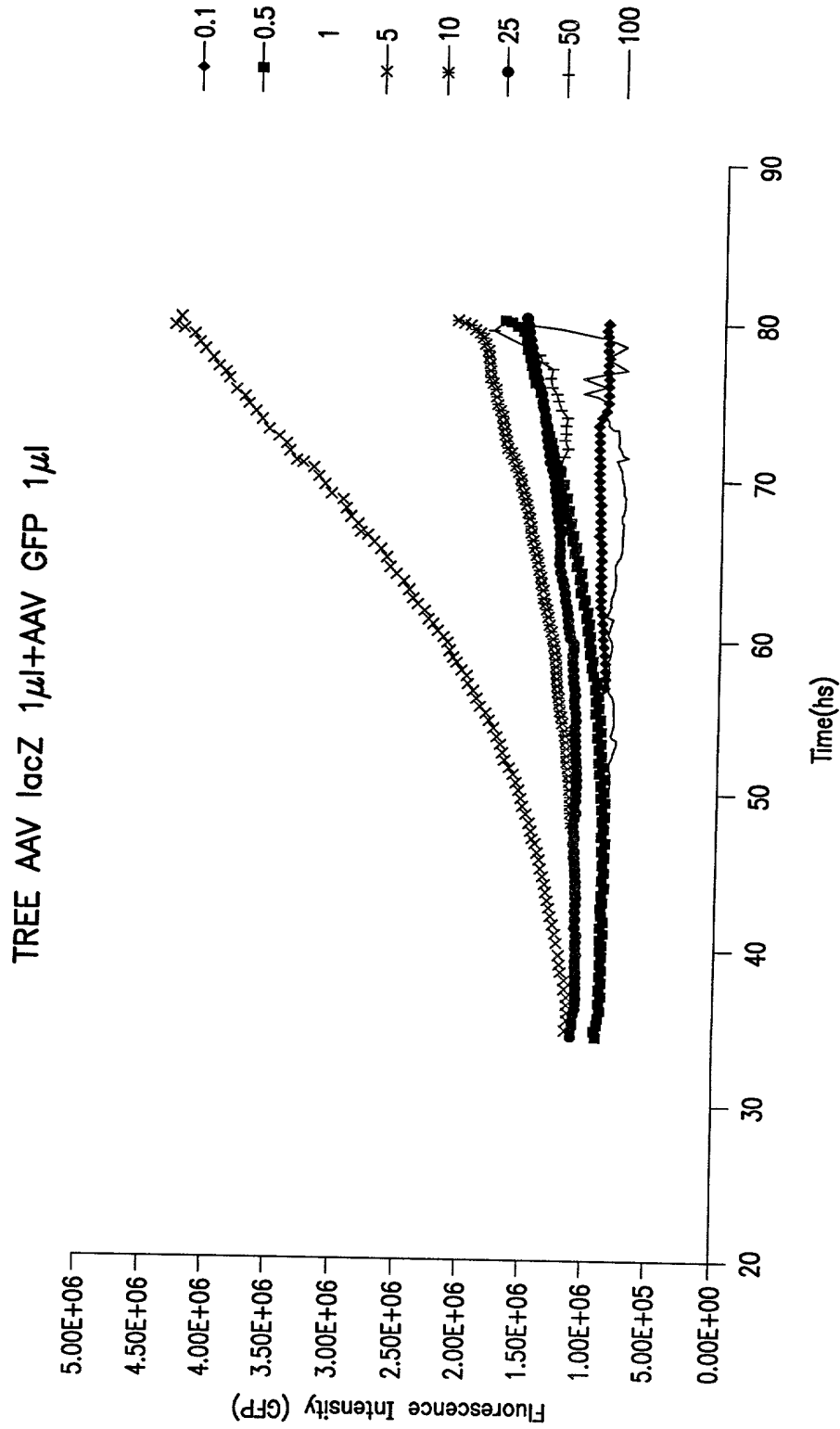


FIG. 2B

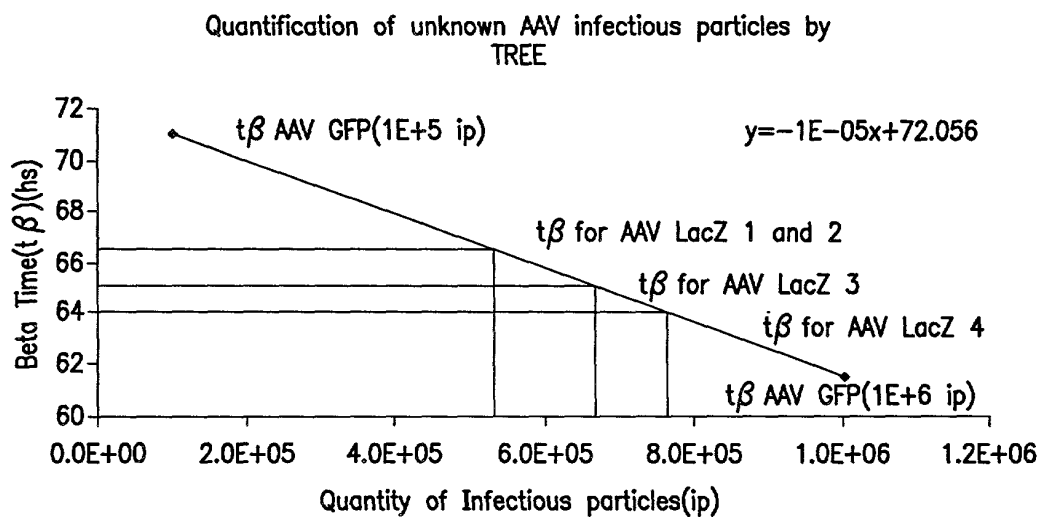


FIG. 2C

Hits on Rep

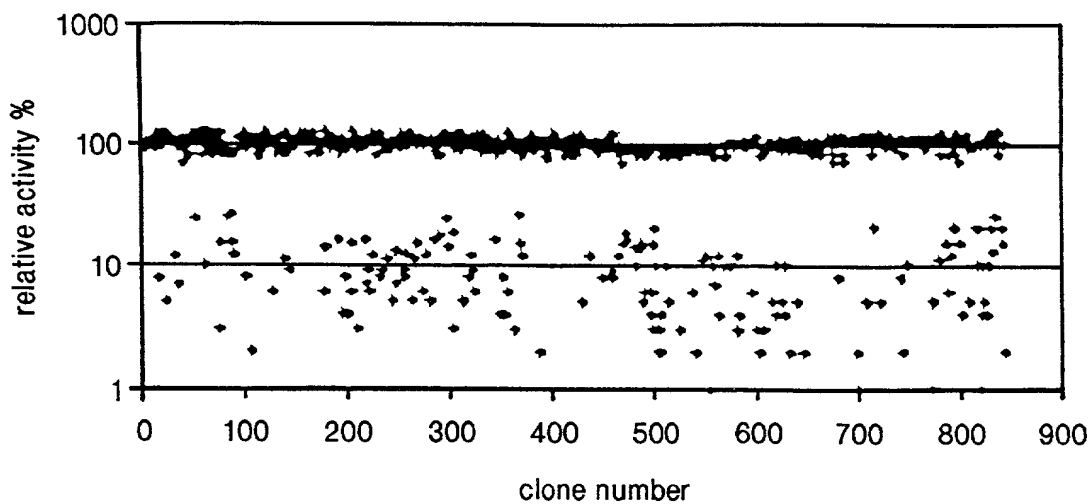


FIG. 3A

Lead positions on Rep

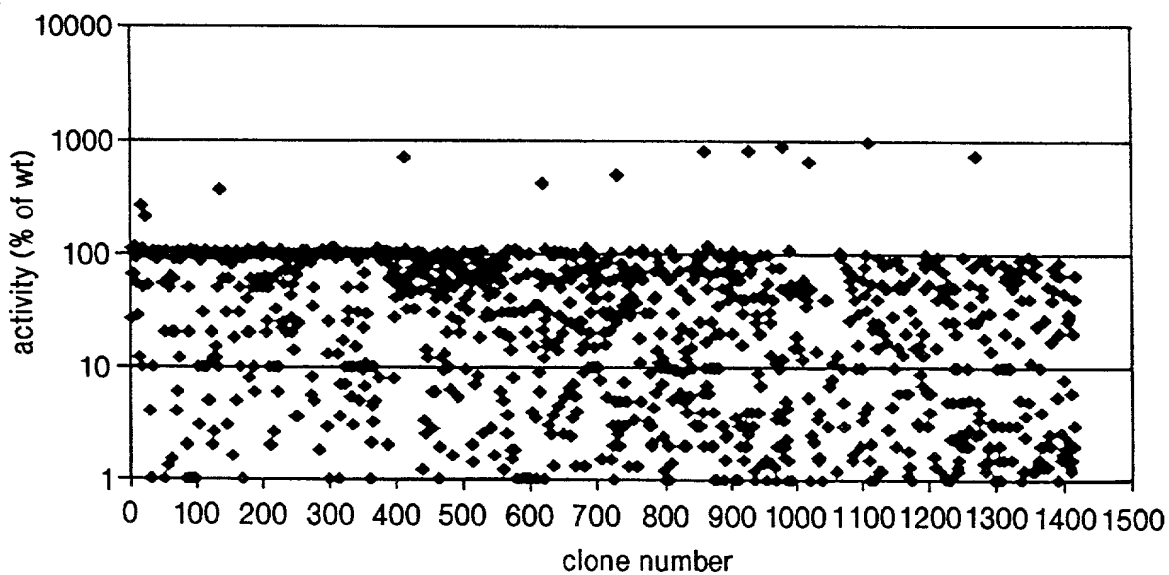


FIG. 3B

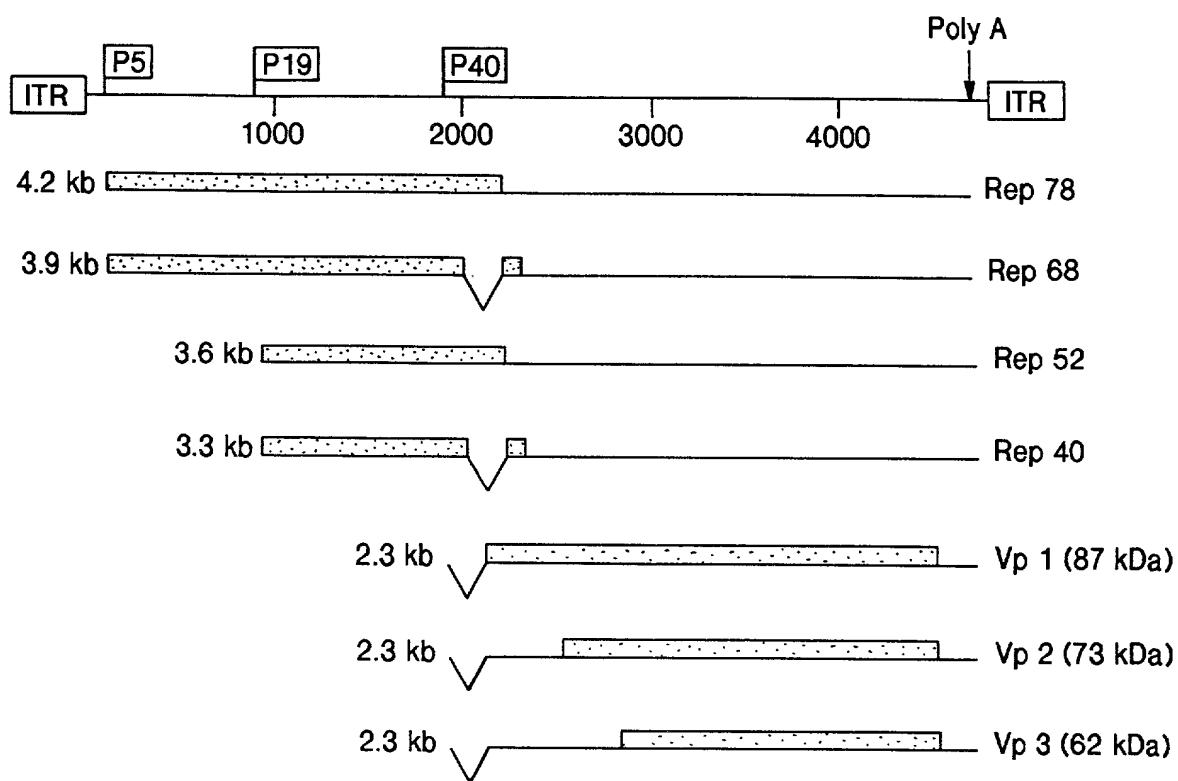


FIG. 4

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      10      20      30      40      50      60
1  MPGFYEIVIKVPSDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ  60
2  MPGFYEIVIKVPSDLDEHLPGISDSFVNWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ  60
3  MPGFYEIVLKVPSDLDEHLPGISNSFVNWVAEKEWELPPDSMDPNLIEQAPLTVAEKLQ  60
4  MPGFYEIVLKVPSDLDEHLPGISNSFVNWVAEKEWELPPDSMDPNLIEQAPLTVAEKLQ  60
5  MPGFYEIVLKVPSDLDEHLPGISDSFVSWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ  60
6  MPGFYEIVIKVPSDLDEHLPGISDSFVNWVAEKEWELPPDSMDLNLIEQAPLTVAEKLQ  60
7  MATFYEIVIVRVPFDVEEHLPGISDSFVDWVTGQIWELPPESDLNLTLVEQPQLTVADRIR  60
C  M**FYE**:*VP*D***HLPGIS+SFV:WV*****WELPP*SD**+*L*EQ**LTVA****
      70      80      90      100     110     120
1  RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHLIVETTGVKSMVLGRFLSQIRDKLVQTI  120
2  RDFLVQWRRVSKAPEALFFVQFEKGESYFHLHLIVETTGVKSMVLGRFLSQIRDKLVQTI  120
3  REFLVEWRRVSKAPEALFFVQFEKGETYFHLHVLITIGVKSMVVGRYVSQIKEKLVTTRI  120
4  REFLVEWRRVSKAPEALFFVQFEKGETYFHLHVLITIGVKSMVVGRYVSQIKEKLVTTRI  120
5  REFLVEWRRVSKAPEALFFVQFEKGDSYFHLHLIVETGVKSMVVGRYVSQIKEKLVTTRI  120
6  RDFLTEWRRVSKAPEALFFVQFEKGESYFHMHVLEVTTGVKSMVLGRFLSQIREKLIQRI  120
7  RVFLYEWNKFSKQ-ESKFFVQFEKGSEYFHLHTLVETSGISSMVLGRYVSQIRAQLVKVV  119
C  R:FL++W***SK**E**FFVQFEKG+:YFH*H:L+ET:G**SMV:GR::SQI::*L*::*

      130     140     150     160     170     180
1  YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQAWATNMEEYISACL  180
2  YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQAWATNMEEYISACL  180
3  YRGVEPQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQAWATNMDDQYLSACL  180
4  YRGVEPQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQAWATNMDDQYLSACL  180
5  YRGVEPQLPNWFVAVTKTRNGAGGGNKVVDDCYIPNYLLPKTQPELQAWATNMDDQYISACL  180
6  YRGIEPTLPNWFVAVTKTRNGAGGGNKVVDECYIPNYLLPKTQPELQAWATNMEEYISACL  180
7  FQGIPEQINDWVAITKVKK--GGANKVVDSGYIPAYLLPKVQPELQAWATNLDEYKLAAL  177
C  **G:EP:***W*A*TK*****GG*NKVV:D:*YIP*YLLPK*QPELQAWATN*: :Y:*A*L

      190     200     210     220     230     240
1  NLAERKRLVAQHLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
2  NLAERKRLVAHDLTHVSQTQEQNKENLNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
3  NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
4  NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
5  NLAERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDRGITSEK  240
6  NLTERKRLVAQHLTHVSQTQEQNKENQNPNSDAPVIRSKTSARYMELVGWLVDKGITSEK  240
7  NLEERKRLVAQFLAESSQRS-QEAASQREFSADPVIKSKTSQKYMALVNWLVEHGITSEK  236
C  NL+ERKRLVA**L***SQ***Q*****S**PVI*SKTS**YM*LV*WLV**GITSEK

      250     260     270     280     290     300
1  QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPPAPPADIKTNR IYR  300
2  QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMALTKSAPDYLVGPPAPPADIKTNR IYR  300
3  QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ  300
4  QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGSNPPEDITKNRIYQ  300
5  QWIQEDQASYISFNAASNSRSQIKAALDNASKIMSLTKTAPDYLVGQNPPEDISSNRIYR  300
6  QWIQEDQASYISFNAASNSRSQIKAALDNAGKIMSLTKTAPDYLVGQPPVEDISSNRIYK  300
7  QWIQENQESYLSFNSTGNSRSQIKAALDNATKIMSLTKSAVDYLVGSSVPEDISKNR IYWQ  296
C  QWIQE*Q*SY*SFN***NSRSQIKAALDNA:KIM+LTK:A*DYLVG: :**+DI: :NRI*:

      310     320     330     340     350     360
1  ILELNGYEPAYAGSVFLGWAQKRFGRNTIWLFGPATGKTNIAEAIHAHVPPFYGCVNWT  360
2  ILELNGYDPAYAGSVFLGWAQKRFGRNTIWLFGPATGKTNIAEAIHAHVPPFYGCVNWT  360
3  ILELNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATGKTNIAEAIHAHVPPFYGCVNWT  360
4  ILELNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATGKTNIAEAIHAHVPPFYGCVNWT  360
5  ILEMNGYDPQYAASVFLGWAQKKFGKRNTIWLFGPATGKTNIAEAIHAHVPPFYGCVNWT  360
6  ILELNGYDPQYAASVFLGWATKKFGKRNTIWLFGPATGKTNIAEAIHAHVPPFYGCVNWT  360
7  IFEMNGYDPAYAGSILYGWCQRSFNKRNTVWLYGPATGKTNIAEAIHAHVPPFYGCVNWT  356
C  I*E+NGY*P:YA:S***GW***:F*KRNT*WL*GPATGKTNIAEAIHAHVPPFYGCVNWT
  
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FIG. 5A

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      370      380      390      400      410      420
1  NENFPFND CVDKMVIWEEGKMTAKVVESAKAILGGSKVRVDQCKSSAQIDPTPVI VTS 420
2  NENFPFND CVDKMVIWEEGKMTAKVVESAKAILGGSKVRVDQCKSSAQIDPTPVI VTS 420
3  NENFPFND CVDKMVIWEEGKMTAKVVESAKAILGGSKVRVDQCKSSAQIEPTPVI VTS 420
4  NENFPFND CVDKMVIWEEGKMTAKVVESAKAILGGSKVRVDQCKSSAQIEPTPVI VTS 420
5  NENFPFND CVDKMVIWEEGKMTAKVVESAKAILGGSKVRVDQCKSSAQIDPTPVI VTS 420
6  NENFPFND CVDKMVIWEEGKMTAKVVESAKAILGGSKVRVDQCKSSAQIDPTPVI VTS 420
7  NENFPFND CVDKMLIWEEGKMTNKVVESAKAILGGSKVRVDQCKSSVQIDSTPVI VTS 416
C  NENFPFND CVDKM*IWEEGKMT*KVVESAKAILGGSKVRVDQCKSS*QI+*TPVI VTS
      430      440      450      460      470      480
1  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDGKVTQKEVKEFFRWAQDHVTEV 480
2  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDGKVTQKEVKEFFRWAQDHVTEV 480
3  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDGKVTQKEVKDFFRWASDHVTDV 480
4  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDGKVTQKEVKDFFRWASDHVTDV 480
5  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDGKVTQKEVKDFFRWASDHVTEV 480
6  NTNMC AVIDGNSTTFEHQQPLQDRMFKFELTRRLDHDGKVTQKEVKDFFRWAKDHVVEV 480
7  NTNMC VVDGNSTTFEHQQPLEDRMFKFELTRRLDHDGKVTQKEVKDFFAWAKVNQVPV 476
C  NTNMC *V* DGNSTTFEHQQPL*DRMFKFELT+RL:*DFGK*TKQEVK+FF*WA:***+:V

      490      500      510      520
1  AHEFYVRKGGANKRPAPDDADKSEPKRA-----CPSVADPSTSDAEG 522
2  AHEFYVRKGGANKRPAPDDADKSEPKRA-----CPSVADPSTSDAEG 522
3  AHEFYVRKGGAKKR PASNDADVSEPKRQ-----CTSLAQPTTSDAEA 522
4  AHEFYVRKGGAKKR PASNDADVSEPKRQ-----CTSLAQPTTSDAEA 522
5  THEFYVRKGGARKRPAPNDADISEPKRA-----CPSVAQPSTSDAEA 522
6  EHEFYVRKGGAKKR PASDADISEPKRV-----RESVAQPSTSDAEA 522
7  THEFKVPRELAGTKGAEKSLKRPLGDTVNTSYKSLEKRARLSFVPETPRSSDVTVDPAPL 536
C  :HEF*V+***A:***A:****.*****:
                                     +:***:***A*:

      530      540      550      560      570      580
1  APVDFADRYQNKCSRHAGMLQMLFPCKTCERMNQNFNICFTHGTRDCSECFP--GVSESQ 580
2  APVDFADRYQNKCSRHAGMLQMLFPCKTCERMNQNFNICFTHGTRDCSECFP--GVSESQ 580
3  P-ADYADRYQNKCSRHVGMNLMFLFPCKTCERMNQISNVCFTHGQRDCGECFPGMSESQPV 581
4  P-ADYADRYQNKCSRHVGMNLMFLFPCKTCERMNQISNVCFTHGQRDCGECFPGMSESQPV 581
5  P-VDYADRYQNKCSRHVGMNLMFLPCRQ CERMNQNV D ICFTHGVMDCAECFP-VSESQPV 580
6  S-INYADRYQNKCSRHVGMNLMFLPCRQ CERMNQNSN ICFTHGQKDCLECFP--VSESQP 579
7  RPLNWN SRYDCKCDYHAQFDNISNKCDECEYLNRGKNGCICHNVTHCQICHG----- 588
C  ::::+**RY**KC**H:***:***C::CE**N*:::C**H*::*C.*C**...::+:::

      590      600      610      620
1  PVVRKR TYRKLCAIHLLGRAPEIACSACDLVNVDLDDCVSEQ 623
2  PVVRKR TYRKLCAIHLLGRAPEIACSACDLVNVDLDDCVSEQ 623
3  SVVKKK TYQKLCPIHHILGRAPEIACSACDLANVDLDDCVSEQ 624
4  SVVKKK TYQKLCPIHHILGRAPEIACSACDLANVDLDDCVSEQ 624
5  SVVRKR TYQKLCPIHHIMGRAPEVACSACELANVDLDDCDMEQ 623
6  VSVVKK KAYQKLCYIHHIMG-KVPDACTACDLVNVDLDDCIFEQ 621
7  -----IPPWEKENLSDFGDFDDANKEQ 610
C  :+*:*:*:*:*:*:*:*:*:*:*:*:*:*:*D*DD*:EQ

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FIG. 5B